

SEQ ID NO: 1

CAAAAACAGAACAGAAAGCAGGACGTGAGACTTCTACCTGCTCACTCAGAACATCATTCT 60
GCACCAACCATGGCCACGTTGTGGAGCTCAGTACCAAAGCCAAGATGCCATTGTGGC 120
5 CTGGGCACTTGGAAGTCTCCTCTCGCAAAGTGAAAGAAGCAGTGAAGGTGGCATTGAT 180
GCAGGATATCGGCACATTGACTGTGCCTATGTCTATCAGAACATGAAGTGGGGAA 240
GCCATCCAAGAGAACATCCAAGAGAACGGCTGTGAAGCGGGAGGACCTGTCATCGTCAGC 300
AAGTTGTGGCCCACCTCCAGATCGAGAACGCTCTGAACAAACCTGGACTGAAATATAAAC 360
10 CAGTGACTAACCAAGGTTGAGTGTACCCATACCTCACGCAGGAGAAACTGATCCAGTACT 420
GCCACTCCAAGGGCATCACCGTTACGGCCTACAGCCCCCTGGCTCTCCGGATAGACCTT 480
GGGCCAAGCCAGAACGACCCCTCCCTGCTGGAGGATCCAAGATTAAGGAGATTGCTGCAA 540
AGCACAAAAAACCGCAGCCCAGGTTCTGATCCGTTCCATATCCAGAGGAATGTGATTG 600
TCATCCCCAAGTCTGTGACACCAGCACGCATTGTTGAGAACATTCAAGGTCTTGACTTTA 660
AATTGAGTGATGAGGAGATGGCAACCATACTCAGCTAACAGAAACTGGAGGGCCTGTA 720
15 ACGTGTGCAATCCTCTCATTGGAAGACTATCCCTCGATGCAGAACATTGAGGTTGAA 780
TCTCCTGGTGAGATTATACAGGAGATTCTCTTCGCTGAAGTGTGACTACCTCCACT 840
CATGTCCCATTAGCCAAGCTTATTAAAGATCACAGTGAACCTAGTCCTGTTATAGACG 900
AGAATCGAGGTGCTGTTAGACATTATTCGTATGTTCAACTAGGATCAGAACATCA 960
CAGAAAAGCATGGCTTGAATAAGGAAATGACAATTTCACCTATCTGATCAGAACAA 1020
20 ATGTTTATTAAGCATCAGAAACTCTGCCAACACTGAGGATGAAAGATCAATAAAAAAA 1080
TAATAATCAT 1090

SEQ ID NO: 2

Met	Ala	Thr	Phe	Val	Glu	Leu	Ser	Thr	Lys	10	
5	Ala	Lys	Met	Pro	Ile	Val	Gly	Leu	Gly	Thr	20
Trp	Lys	Ser	Pro	Leu	Gly	Lys	Val	Lys	Glu	30	
Ala	Val	Lys	Val	Ala	Ile	Asp	Ala	Gly	Tyr	40	
Arg	His	Ile	Asp	Cys	Ala	Tyr	Val	Tyr	Gln	50	
Asn	Glu	His	Glu	Val	Gly	Glu	Ala	Ile	Gln	60	
10	Glu	Lys	Ile	Gln	Glu	Lys	Ala	Val	Lys	Arg	70
Glu	Asp	Leu	Phe	Ile	Val	Ser	Lys	Leu	Trp	80	
Pro	Thr	Ser	Arg	Ser	Arg	Ser	Ser			88	

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SEQ ID NO: 3

CAAAAACAGCAACAGAAAGCAGGACGTGAGACTTCTACCTGCTCACTCAGAATCATTCT 60
GCACCAACCATGGCCACGTTGTGGAGCTCAGTACCAAAGCCAAGATGCCATTGTGGC 120
5 CTGGGCACTTGGAAGTCTCCTCTCGCAAAGTGAAAGAACAGTGAAGGTGGCATTGAT 180
GCAGGATATCGGCACATTGACTGTGCCTATGTCTATCAGAATGAACATGAAGTGGGGAA 240
GCCATCCAAGAGAACAGATCCAAGAGAACGGCTGTGAAGCGGGAGGACCTGTCAGC 300
AAGTTGTGGCCCACTTCTTGAGAGACCCCTGTGAGGAAAGCCTTGAGAACAGCC 360
AAGGACCTGAAGCTGAGCTATCTGGACGTCTATTCACTGCCACAGGGATTCAAG 420
10 TCTGGGATGACCTTCCCAAAGATGATAAAGGTAATGCCATCGGTGGAAAAGCAACG 480
TTCTGGATGCCTGGGAGGCCATGGAGGAGCTGGTGGATGAGGGGCTGGTAAAGCC 540
GGGTCTCCAATTCAGCCACTCCAGATCGAGAACGCTCTGAACAAACCTGGACTGAAA 600
TATAAACCAAGCTGACTAACCAAGGGTGGAGTGTACCCATACTCACCGCAGGAGAACTGATC 660
CAGTACTGCCACTCCAAGGGCATCACCGTTACGGCTACAGCCCCCTGGCTCTCCGGAT 720
15 AGACCTGGCCAAGCCAGAACGCCCTCCCTGCTGGAGGATCCAAAGATTAAGGAGATT 780
GCTGCAAAGCACTCCCCAAGTCTGTGACACCAGCACGCATTGTTGAGAACATTCAAGGTCT 840
TTGACTTTAAATTGAGTGATGAGGAGATGGCAACCATACTCAGCTTCAACAGAAACTGGA 900
GGGCCTGTAACGTGTTGCAATCCTCTCATTGGAAGACTATCCCTCGATGCAGAATATT 960
GAGGTTGAATCTCCTGGTGAGATTATACAGGGAGATTCTCTTCCTCGCTGAAGTGTGACT 1020
20 ACCTCCACTCATGTCCCATTAGCCAAGCTTATTAAAGATCACAGTGAACCTAGTCCTG 1080
TTATAGACGAGAACATGGAGGTGCTGTTAGACATTATTCTGTATGTTCAACTAGGATC 1140
AGAATATCACAGAAAAGCATGGCTTGAATAAGGAAATGACAATTTCACCTATCTGA 1200
TCAGAACAAATGTTATTAAGCATCAGAAACTCTGCCAACACTGAGGATGAAAGATCAA 1260
TAAAAAAAATAATAATCAT 1279

SEQ ID NO: 4

	Met	Ala	Thr	Phe	Val	Glu	Leu	Ser	Thr	Lys	10
5	Ala	Lys	Met	Pro	Ile	Val	Gly	Leu	Gly	Thr	20
	Trp	Lys	Ser	Pro	Leu	Gly	Lys	Val	Lys	Glu	30
	Ala	Val	Lys	Val	Ala	Ile	Asp	Ala	Gly	Tyr	40
	Arg	His	Ile	Asp	Cys	Ala	Tyr	Val	Tyr	Gln	50
	Asn	Glu	His	Glu	Val	Gly	Glu	Ala	Ile	Gln	60
10	Glu	Lys	Ile	Gln	Glu	Lys	Ala	Val	Lys	Arg	70
	Glu	Asp	Leu	Phe	Ile	Val	Ser	Lys	Leu	Trp	80
	Pro	Thr	Phe	Phe	Glu	Arg	Pro	Leu	Val	Arg	90
	Lys	Ala	Phe	Glu	Lys	Thr	Leu	Lys	Asp	Leu	100
	Lys	Leu	Ser	Tyr	Leu	Asp	Val	Tyr	Leu	Ile	110
15	His	Trp	Pro	Gln	Gly	Phe	Lys	Ser	Gly	Asp	120
	Asp	Leu	Phe	Pro	Lys	Asp	Asp	Lys	Gly	Asn	130
	Ala	Ile	Gly	Gly	Lys	Ala	Thr	Phe	Leu	Asp	140
	Ala	Trp	Glu	Ala	Met	Glu	Glu	Leu	Val	Asp	150
	Glu	Gly	Leu	Val	Lys	Ala	Leu	Gly	Val	Ser	160
20	Asn	Phe	Ser	His	Phe	Gln	Ile	Glu	Lys	Leu	170
	Leu	Asn	Lys	Pro	Gly	Leu	Lys	Tyr	Lys	Pro	180
	Val	Thr	Asn	Gln	Val	Glu	Cys	His	Pro	Tyr	190
	Leu	Thr	Gln	Glu	Lys	Leu	Ile	Gln	Tyr	Cys	200
	His	Ser	Lys	Gly	Ile	Thr	Val	Thr	Ala	Tyr	210
25	Ser	Pro	Leu	Gly	Ser	Pro	Asp	Arg	Pro	Trp	220
	Ala	Lys	Pro	Glu	Asp	Pro	Ser	Leu	Leu	Glu	230
	Asp	Pro	Lys	Ile	Lys	Glu	Ile	Ala	Ala	Lys	240
	His	Ser	Pro	Ser	Leu						245